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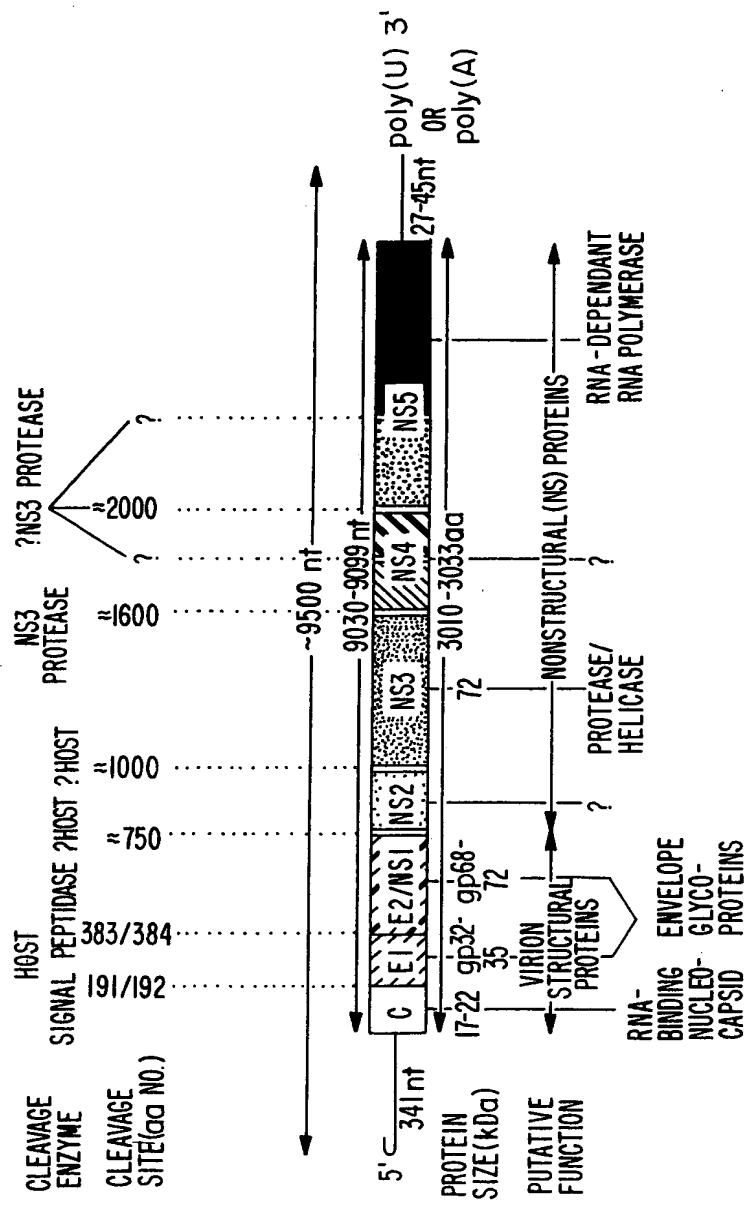


FIG. I



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Consensus

re3 (15-45)
 hcj7.pep (15-45)
 ny1.pep (15-45)
 GE11.2 (15-45)
 s71957.p (15-45)
 ec10 (15-45)
 sp2.tc (15-45)
 M2.2 (15-45)
 reia (15-45)
 168 (15-45)
 M1.5 (15-45)
 hpcprcla.p1 (14-44)
 gm2.tc (15-45)
 s71864.p1 (15-45)
 i15.tc (15-45)
 sp1.tc (15-45)
 re37b (15-45)
 re39 (15-45)
 hpchcj2.p (15-45)
 hpccgenom.p1 (15-45)
 hpcprc4a.p2 (14-44)
 hpcprc11a.p1 (4-34)
 re72b (15-45)
 hpcprc3a.p1 (4-34)
 re70 (15-45)
 re42 (15-45)
 63 (15-45)
 hcvj (15-45)
 hcvj1 (15-45)
 re38 (15-45)
 bk (15-45)
 re5 (15-45)
 re35 (15-45)
 re36 (15-45)
 re54 (15-45)
 re56 (15-45)
 64 (15-45)
 re62 (15-45)
 re41 (15-45)
 hpcvjk3.p (15-45)
 jk2 (15-45)
 hcv1 (15-45)
 us5.tc (15-45)

.T.VTGG.AARTT.G..SLF..G.SQ.IQLI	31
A.YA..AAQGHA.NSFV..RS.A..NLK.V	45
S.Q...Q..H.VR.VA.I.SP.SR.D.S.	45
S.R...QQG.AVH.IA..SL.A..K..V	45
S.H.M.AQQG.VAK.FT..GP.PA.K..	45
S.H..AVQGHSIR.LT..TS.PA.K..V	45
E.H...I..K..ASLTG..NL.AK.N...	45
E.H...N.G.AAA.IAG..TL.AK.NV..	45
Q.R..T..QS.ARIAG..SL.AR.N..	45
Q.H.M..T.G.NAY.LT.FLSV.A..K..	45
E.H.M..A.SS..YRFA..TS.PA.K..V	45
E.H..S..S..ATFSK..MP.A..N..	45
G.TRV..A...SSFA..LTH.P..N..V	44
G.H...A..DAFRFS..TR.P..N..	45
A.NM..AP...YKLTT..SY.A..K..	45
HNH...TS..N.F.ITT..TQ.P..KL..V	45
G.H..A..NAHSLT..LAP.A..K..	45
T.R.S..T..H..A.LT..SP.PR.N.H.V	45
T.H.S..T.G..ASLT.F.AP.A..R..V	45
T.H..ATGH..S.IA..LP.A..K..	45
D.YAS..AQG.S.L.FT..TP.A..K..	45
D.YAS..A.G.A.Y.IT..AP.A..N..	44
R.YAS..A.G..H.FT..ST.AR.N..	34
Q.Y...K..Q.VS.FTG..SS.P..K..	45
D.Y.S..A..SIS.FT..TP.A..K..V	34
S.Y...E.S..R.FA..TL.S..K..	45
N.Y...S.G.AVA.FAG.LQP.AK.NV..	45
H.R..QV.FR.H.LV..TQ.P..K..V	45
H.H..RV.SS.QSLV.WLSQ.P..K..V	45
H.R..VQGHV.STLT..RP.A..K..V	45
N.R..VQG.D.S.LV..SL.P..K..V	45
D.H..AQ.K..NRLV.M.AS.P..K..	45
E.H..AS..QRFT.F.DL.P..K..V	45
T.YM..AN..Q.FV..TP.PA.K..V	45
E.H..TS..Q.FV..SA.A..K..V	45
G.H..Q...QSFT..SP.PQ.K..	45
R.H..K..H..K.FA..TP.P..N..	45
E.R..AVQGHHGAL.LA..TP.P..K..	45
E.R..AI.G..ASSFAG..TS.A..K..V	45
E.R..QQVG...QSLT..TP.P..T..	45
Q.R..AQVG..SSLT..TP.P..N..V	45
R.Q..AQ.GH..S.LA..TP.P..K..V	45
E.H..S.GH.VS.FV..LAP.AK.NV..	45
E.H..S.GH.VT.IA..TS.AK.N..	45

FIG. 2A



i21, tc (15-45)
 M3, i (15-45)
 H77 (15-45)
 re43 (15-45)
 Ge6, 3 (15-45)
 C011 (15-45)
 TH (15-45)
 0115 (15-45)
 re4a (15-45)
 q1 (15-45)
 q3 (15-45)
 gh1, tc (15-45)
 M4, i (15-45)
 nac5, tc (15-45)
 hpcgenanti, p3 (15-45)
 hcj4 (15-45)
 hpchcv, p2 (15-45)
 hcj1 (15-45)
 hct18 (15-45)
 hct27 (15-45)
 hcve1 (15-45)
 ge12 (15-45)
 LG (15-45)
 jt, p3, x (15-45)
 us4, tc (15-45)
 jk1 (15-45)
 hpcvjk4, p (15-45)
 hpce2cor, p (15-45)
 hpcns34d, p (15-45)
 FT0, 1 (15-45)
 Gj6, 1 (15-45)
 re7 (15-45)
 hcvkf (16-46)
 arg2, tc (15-45)
 hcj6 (15-45)
 hpchcj5, p (15-45)
 rs1, pep (15-45)
 re71 (15-45)
 re6 (15-45)
 hcj8, pep (15-45)
 re40 (15-45)
 hpcencr, p (15-45)
 re55b (15-45)
 aus1, tc (15-45)
 PC2, i (15-44)
 hct23 (15-45)
 re34 (15-45)

S.H...T.H.VA.FS...TV.PK.N...
 E.H...A.Y.AA.LA..TS.AK.N...
 E.H...S.G..A.LVG.LTP.AK.N...
 G.H...S.G.A.A.IAG.LTP.AR.N...V
 K.H...S.S.IA..LTP.AK.NV...
 K.Y...SQ.QA.F.FT..LQQ.AK.N...
 E.T...S.HGAL.IA..NQ.AR.N...
 E.Y...AS.S.FTLVG.KQ.SQ.N...V
 Q.Y.S.SSG..S.LV.I.SP.A..NL...
 E.Y.S.A.Q.AR.FAGF.QS.AK.N...
 E.Y.S.S.Q.A.FVR..ET.PK.N...
 S.Y.S.AQ.AAQ.IT..SR.S.K...V
 S.Y.TQG.AAS.LT..SA.A.N...
 N.Y.S.T.GH.GH.LTA..SP.A.N...
 S.I.S.TV...HSLA..TQ.A.K...
 E.YTS.A.SH..STLA..SP.A.R...V
 H.LT..H.L.S.FAG..TP.P.R...
 E.I.S.Q.AMS.LV..TP.AK.N...
 E.YTS.N.GH.MT.IVRF.AP.PK.NVH...
 T.YT..N.QALT.F.SP.AK.D...
 E.YT..ST.Q.LV..SR.AK.D...
 A.YTS.S.Q.FA..SL.SQ.K...V
 A.YT..SV.H.FS..SQ.AK.N...
 V.YT..SQ.H.QSVT.F.TQ.PA.R...
 H.YT..TV.S.Q.LVGFLSP.P.N...
 T.Y.SV.H.SQ.RRVA.F.SP.SA.K...V
 T.T.S.H.SQI.R.VT.F.SP.SA.K...V
 K.SL..VTR..AAARLTA..SS.P.R...
 G.SL..AR.AAS.LAG..SS.P.R...
 V.Q.SPPQ.GY..SVLTGILSP.AK.N...V
 V.Q.S.Q.GY..SVLTGILSP.AK.N...V
 G.YTV..AS.F..SRLT..AL.P.R...V
 N.HTV..TEGFA.QRLT..AL.P.K...
 S.RTA..AQ.FN.Y.VA.I.SP.P.R...V
 Q.HTV..ST.HNARTLTGM.SL.AR.K...
 N.RTV.A.S.A.R.FT.M.SS.SK.NL...
 Q.RTV..QVGHHSV.R.FT..SA.SA.N...
 E.HT..AVSGH..NVLT..SS.S.N...
 V.RT..EV..ANTFA..TT.P.N..I...
 T.YSS.QE.G..VA.FAG..TT.AK.NLY...
 S.S.V..RQ.SA.FRFT.F.SR.PT.E.K...
 N.YT.A.SM.QSIYRLTDI..ST.P.KL..V
 R.ILMA.RQ.EV.QSFPG..SLAP..K.H...
 D.YA..SV.SIMA.IARF.SP.AR.D...
 E.YA..AS.GHDVSSFAR..AP.AR.N...-
 E.HR..S.S.A.VA..TP.AR.N...
 N.RAV.MVQS..YALT..DS.AA.KL..V

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Hutchinson	Strains:	395	407	
H77	384ETHVTGGSAGRTTAGLVGLLTPGAKQNIQLI	41		1977
H90	-----SVL-TASF--R-P-----			1990
HC-J4	Strains:	395	407	
HPCJ483	384ETYTGGAASHTTSTLASLFSPGASQRIQLV	414	1983	
J48711	A-----V-----RFT-----S-----			
J48712	A-----AV-----RFT-F-----S-----			
J48713	A-----AV-----RFT-----S-----			1987
J48714	A-----AV-----GFT-----S-----			
J48715	-----RV-G-----GFT-----S-----			
HPCJ491	A-----V-GR-----GFT-----S-----K-----			
J49120	-----H-T-RV-G-----RFT-----S-----K-----			
J49121	-----H-T-RVVG-----GFT-----S-----K-----			1991
J49122	-----H-T-RV-GR-----GFT-----S-----K-----			
J49126	T-----V-GR-----GFT-----S-----K-----			
J49127	K-----RFT-----			
NY	Strains:	395	407	
NY1.1	384STRVTGGQQGRAVHGIASLFLSLGASQKIQLV	414	t0	
NY1.2	-----Q-F-----R-----E-----			
NY1.3	-----	N-----		
NY2.1	-----H-A-SLT-----R-----N-----			6mo
NY2.2	-----H-A-SLT-----R-----N-----			
NY3.1	N-----R-----A-SLT-----P-----N-----			
NY3.2	N-----R-----A-SLT-----P-----N-----			-8mo
NY3.3	G-----R-----A-SLT-----P-----EN-R-----			
NY3.4	S-----A-SLT-----T-----N-----			
NY3.5	-----H-----AL-----AY-----T-FL-H-P-----			
NY4.1	-----Q-M-----AYSL-----L-P-----N-----			
NY4.2	-----Q-M-----AYSL-----LGP-----			14mo
NY4.3	-----Q-M-----AYSL-----L-P-----			
RS	Strains:	395	407	
RS1.1	384RTRTVGGQVGHSVRGFTSLFSAGSAQNIQLI	414	t0	
RS1.2	Q-----			
RS1.3	Q-----	D-----		
RS2.4	Q-----	L-----		2mo
RS3.1	Q-----	L-----		6mo
RS4.1	Q-----M-G-----L-----R-----			
RS4.2	Q-H-----M-G-----L-----			8mo
RS5.1	Q-H-----M-G-----L-N-----			11mo

FIG. 3



Amino Acid Position:

FIG. 4

% Conserved AA Character for Each AA Position:

49 99 58 100 100 97 73 77 100 75 90 100 63 89 100 93 100 99 99 100 87 87 100 100

Legend

##	99-100% <u>identical</u> amino acids (invarantly conserved)
##	100% conserved amino acid substitutions (invarantly conserved)
#	90-99% conserved amino acid substitutions
a	80-89% conserved amino acid substitutions
#	70-79% conserved amino acid substitutions
*	49-69% conserved amino acid substitutions (highly variable)

Notes:

Positions 403 (F, L); 400 (R, R) and 407 (R, L), utilized only to eliminate the character, respectively.

Position 394 represents the only strongly conserved basic amino acid, all others conserved for hydrophobic character and/or size in the case of amino acid position 407.

Position 398 appears to be least conserved between AA 395-407 in sequentially temporal HCV isolates in individual patients (see Fig. 3).

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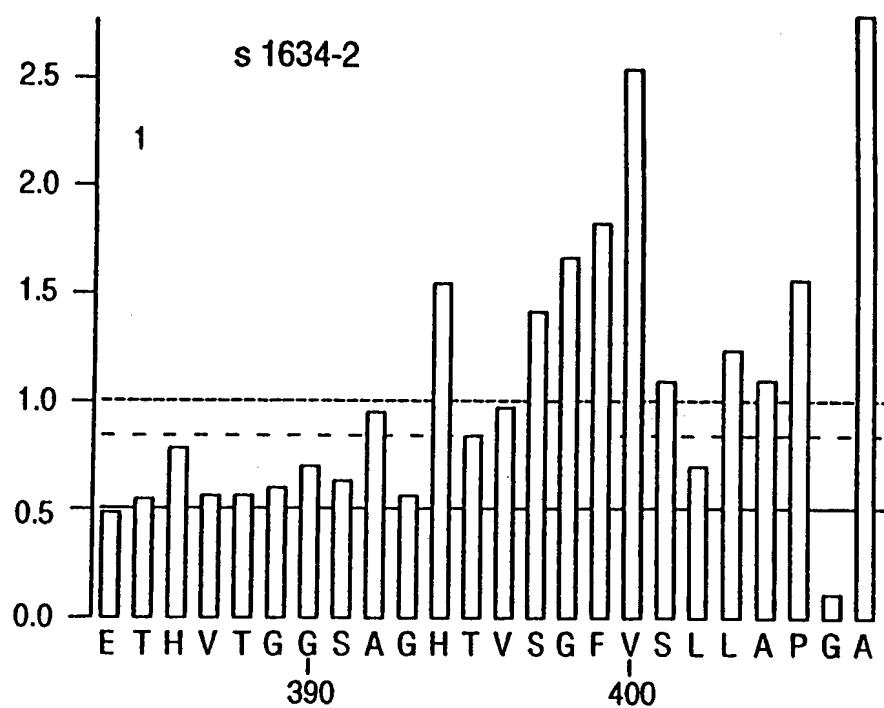


FIG.5A

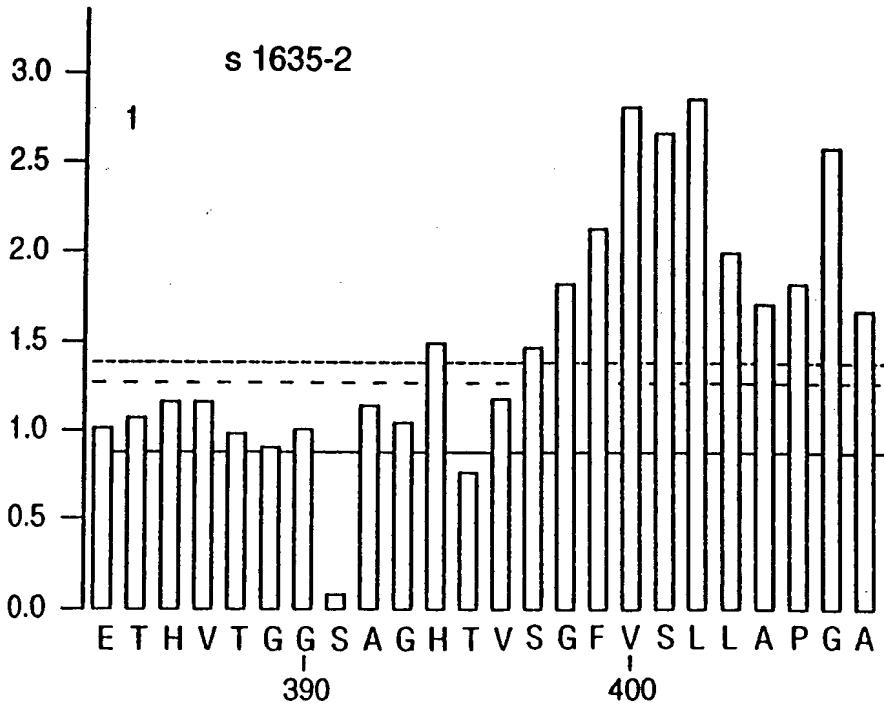


FIG.5B



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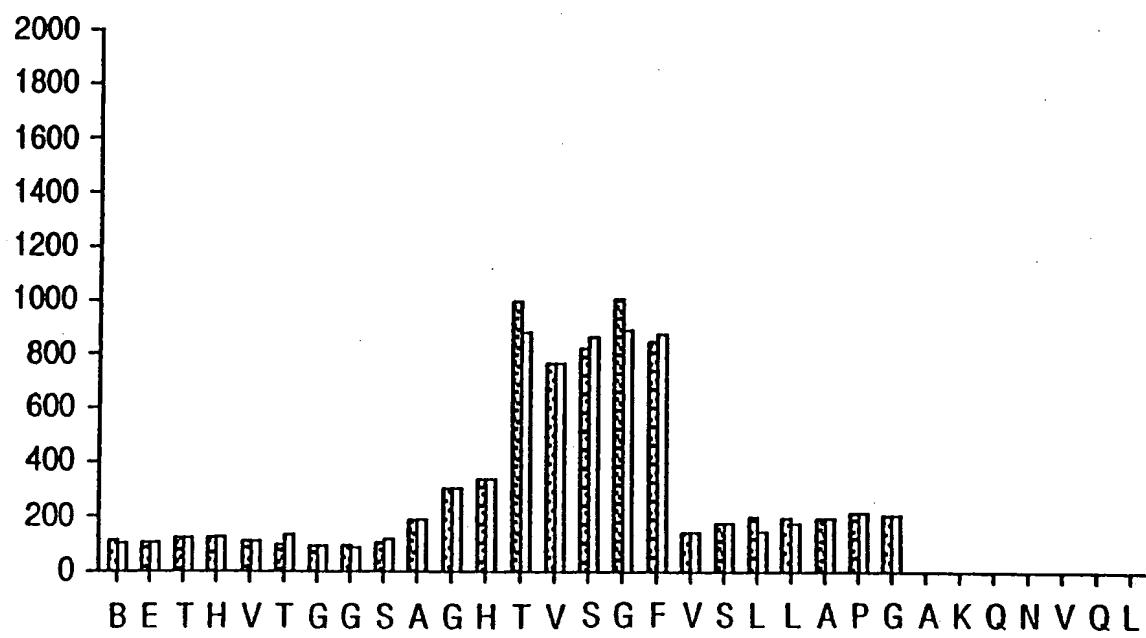


FIG.6

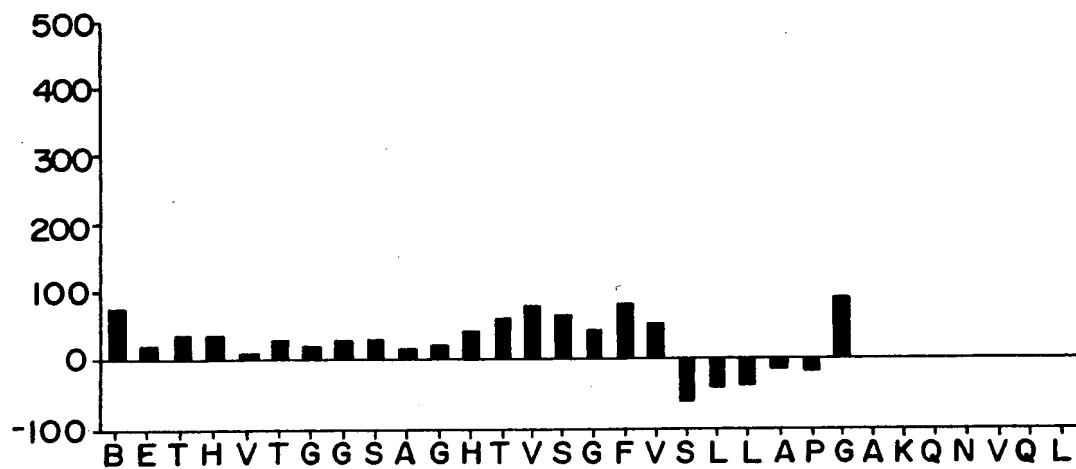


FIG.7A

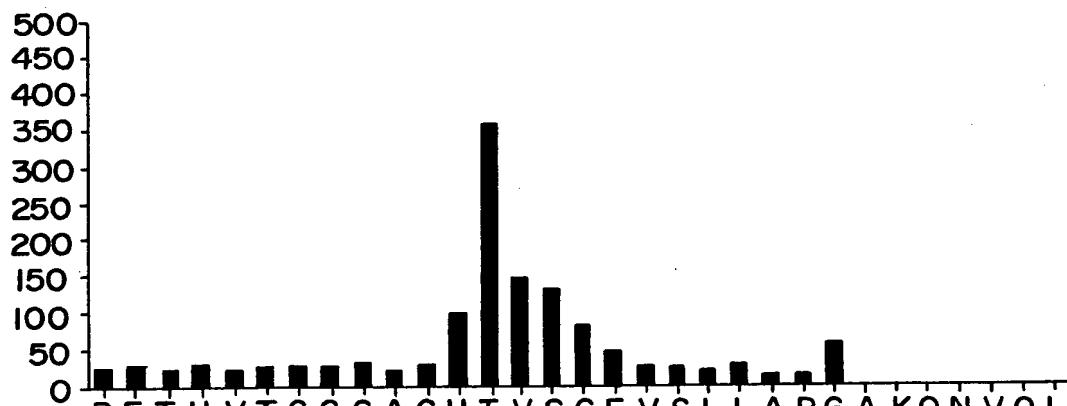


FIG.7B

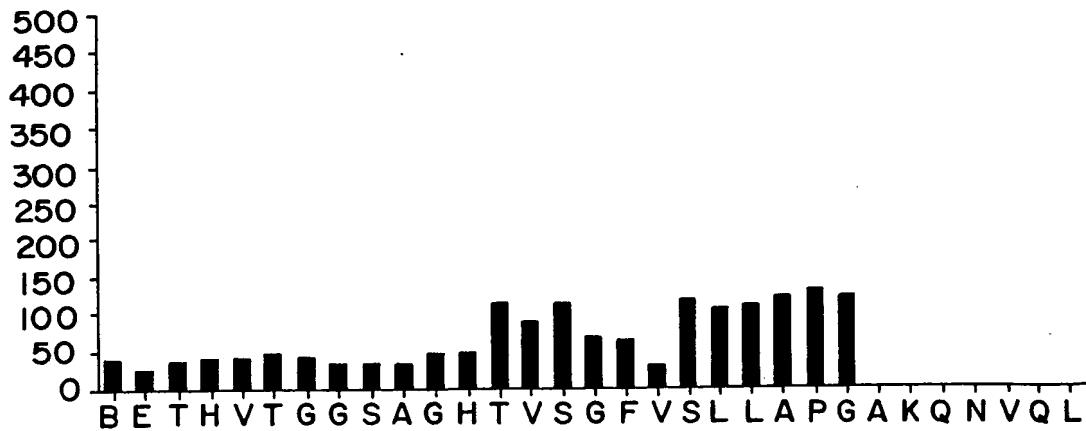


FIG.7C